

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/892,613 D  
Source: IFW/C  
Date Processed by STIC: 10/02/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/09/892,613D

TIME: 08:43:49

Input Set : N:\Crf4\10022006\I892613C.raw

Output Set: N:\CRF4\10102006\I892613D.raw

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1 <110> APPLICANT: Leung, Shawn Shui-on
2 <120> TITLE OF INVENTION: REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY
3   FRAMEWORK-PATCHING
4 <130> FILE REFERENCE: 655
C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/892,613D
6 <141> CURRENT FILING DATE: 2001-06-27
7 <160> NUMBER OF SEQ ID NOS: 71
8 <170> SOFTWARE: PatentIn version 3.3
9
10 <210> SEQ ID NO: 1
11 <211> LENGTH: 369
12 <212> TYPE: DNA
13 <213> ORGANISM: Artificial Sequence
14 <220> FEATURE:
15 <223> OTHER INFORMATION: FR-patched heavy chain variable region sequence (Full DNA
16   Sequence) formed by joining the N- and C- terminal (SEQ 3 and 6)
17   halves at the KpeI site.
18 <220> FEATURE:
19 <221> NAME/KEY: V_region
20 <222> LOCATION: (1)..(369)
21 <400> SEQUENCE: 1
22   gaagtgcagc tgctggagtc tgggggaggc ttagtgcagc ctggagggtc cctgaggctc      60
23   tcctgtgcag cctctggatt ctcttcagt atctatgaca tgccttgggt tcgccaggca      120
24   ccgggaaagg ggctggagtg ggtcgcatat attagtagtg gtggtggtac cacctactat      180
25   ccagacactg tgaaggccg attcaccatc tccagagaca atgccaagaa ctccctgtac      240
26   ctgcaaatga acagtctgag ggtggaggac acagccttat attactgtgc aagacatagt      300
27   ggctacggta gtagctacgg ggttttgttt gcttactggg gccaagggaac tctggtcact      360
28   gtctcttca
29
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 123
32 <212> TYPE: PRT
33 <213> ORGANISM: Chimaera sp.
34 <400> SEQUENCE: 2
35   Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
36   1           5           10           15
37   Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ile Tyr
38           20           25           30
39   Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
40           35           40           45
41   Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
42           50           55           60
43   Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
44           65           70           75           80
45   Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys

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46          85          90          95
47      Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
48          100          105          110
49      Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
50          115          120
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 111
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: N-template is a synthetic sense-strand oligonucleotide
encoding
58      amino acid 14-50 of the VH region (SEQ ID No. 2). The template
59      is PCR-amplified by two primers (SEQ ID No. 4 and 5)
60 <220> FEATURE:
61 <221> NAME/KEY: V_region
62 <222> LOCATION: (1)..(111)
63 <400> SEQUENCE: 3
64      cctggagggt ccctgaggct ctctgtgca gcctctggat tctccttcag tatctatgac
65      atgtcttggg ttcgccaggc accgggaaag gggctggagt ggtcgcata c
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 57
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding
73      amino acid 1-19 of the VH region (SEQ ID No. 2). The 3' end of
74      the primer overlaps with the 5' end of the template by 18
75      nucleotides.
76 <220> FEATURE:
77 <221> NAME/KEY: primer_bind
78 <222> LOCATION: (1)..(57)
79 <400> SEQUENCE: 4
80      gaagtgcagc tgctggagtc tgggggaggc ttagtgcagc ctggagggtc cctgagg
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 48
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: 3' Primer is a synthetic anti-sense-strand oligonucleotide
88      encoding amino acid 43-59 of the VH region (SEQ ID No. 2). The
89      primer overlaps with the template by 21 nucleotides.
90 <220> FEATURE:
91 <221> NAME/KEY: primer_bind
92 <222> LOCATION: (1)..(48)
93 <400> SEQUENCE: 5
94      gtaggtggta ccaccaccac tactaatgta tgcgaccac tccagccc
96 <210> SEQ ID NO: 6
97 <211> LENGTH: 132
98 <212> TYPE: DNA

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Output Set: N:\CRF4\10102006\I892613D.raw

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99 <213> ORGANISM: Artificial Sequence
100 <220> FEATURE:
101 <223> OTHER INFORMATION: C-terminal is a synthetic sense-strand oligonucleotide
encoding
102     amino acid 68-111 of the VH region (SEQ ID No 2) The template is
103     PCR-amplified by two primers (SEQ ID No 7 and 8)
104 <220> FEATURE:
105 <221> NAME/KEY: V_region
106 <222> LOCATION: (1)..(132)
107 <400> SEQUENCE: 6
108     ttcaccatct ccagagacaa tgccaagaac tccctgtacc tgcaaatgaa cagtctgagg      60
109     gtggaggaca cagccttata ttactgtgca agacatagtg gctacggtag tagctacggg      120
110     gttttgtttg ct                                                         132
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 60
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding
118     amino acid 55-74 of the VH region (SEQ ID No 2). The 3' end of
119     the primer overlaps with the 5'end of the template by 21
120     nucleotides.
121 <220> FEATURE:
122 <221> NAME/KEY: primer_bind
123 <222> LOCATION: (1)..(60)
124 <400> SEQUENCE: 7
125     ggtggtacca cctactatcc agacactgtg aagggccgat tcaccatctc cagagacaat      60
127 <210> SEQ ID NO: 8
128 <211> LENGTH: 57
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: 3' Primer is a synthetic anti-sense-strand oligonucleotide
133     encoding amino acid 105-123 of the VH region (SEQ ID No 2). The
134     primer and the template overlaps by 21 nucleotides.
135 <220> FEATURE:
136 <221> NAME/KEY: primer_bind
137 <222> LOCATION: (1)..(57)
138 <400> SEQUENCE: 8
139     tgaagagaca gtgaccagag tcccttggcc ccagtaagca aacaaaaccc cgtagct      57
141 <210> SEQ ID NO: 9
142 <211> LENGTH: 321
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: FR-patched light chain variable region sequence formed by
joining
147     the N- and C- terminal (SEQ 11 and 14) halves at the KpeI site.
148 <220> FEATURE:
149 <221> NAME/KEY: V_region
150 <222> LOCATION: (1)..(321)

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## RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/09/892,613D

TIME: 08:43:49

Input Set : N:\Crf4\10022006\I892613C.raw

Output Set: N:\CRF4\10102006\I892613D.raw

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151 <400> SEQUENCE: 9
152   gatatccaga tgaccagtc tccatcctcc ctgtctgcct ctgtgggaga cagagtcacc      60
153   attagttgca gggcaagtca ggacattagc aattatttaa actggtatca gcagaaacca      120
154   ggtaaggctc cgaaactcct gatctactac actagtatat tacactcagg agtcccatca      180
155   aggttcagtg gcagtgggtc tggaacagaa ttactctca ccattagctc cctgcagcca      240
156   gaagattttg ccacttactt ttgccaacag ggtaatacgc ttccgtggac gttcgggtga      300
157   ggcaccaagg tggaaatcaa a                                           321
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 107
161 <212> TYPE: PRT
162 <213> ORGANISM: Chimaera sp.
163 <400> SEQUENCE: 10
164   Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
165   1             5             10             15
166   Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
167   20             25             30
168   Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
169   35             40             45
170   Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
171   50             55             60
172   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
173   65             70             75             80
174   Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
175   85             90             95
176   Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
177   100            105
179 <210> SEQ ID NO: 11
180 <211> LENGTH: 108
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: N-template is a synthetic sense-strand oligonucleotide
encoding
185   amino acid 11-46 of the VL region (SEQ ID No. 10). The template
186   is PCR-amplified by two primers (SEQ ID No. 12 and 13)
187 <220> FEATURE:
188 <221> NAME/KEY: V_region
189 <222> LOCATION: (1)..(108)
190 <400> SEQUENCE: 11
191   ctgtctgcct ctgtgggaga cagagtcacc attagttgca gggcaagtca ggacattagc      60
192   aattatttaa actggtatca gcagaaacca ggtaaggctc cgaaactc                  108
194 <210> SEQ ID NO: 12
195 <211> LENGTH: 51
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding
200   amino acid 1-17 of the VH region (SEQ ID No 10). The 3' end of
201   the primer overlaps with the 5'end of the template by 21
202   nucleotides.

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## RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/09/892,613D

TIME: 08:43:49

Input Set : N:\Crf4\10022006\I892613C.raw

Output Set: N:\CRF4\10102006\I892613D.raw

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203 <220> FEATURE:
204 <221> NAME/KEY: primer_bind
205 <222> LOCATION: (1)..(51)
206 <400> SEQUENCE: 12
207     gatatccaga tgacccagtc tccatcctcc ctgtctgcct ctgtgggaga c           51
209 <210> SEQ ID NO: 13
210 <211> LENGTH: 40
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: 3' Primer is a synthetic anti-sense-strand oligonucleotide
215     encoding amino acid 40-53. The primer and the template overlaps
216     by 18 nucleotides.
217 <220> FEATURE:
218 <221> NAME/KEY: primer_bind
219 <222> LOCATION: (1)..(40)
220 <400> SEQUENCE: 13
221     atatactagt gtagtagatc aggagtttcg gaggccttacc           40
223 <210> SEQ ID NO: 14
224 <211> LENGTH: 120
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: C-terminal is a synthetic sense-strand oligonucleotide
encoding
229     amino acid 59-98 of the VH region (SEQ ID No 10) The template is
230     PCR-amplified by tow primers (SEQ ID No 15 and 16)
231 <220> FEATURE:
232 <221> NAME/KEY: V_region
233 <222> LOCATION: (1)..(120)
234 <400> SEQUENCE: 14
235     ccatcaaggt tcagtggcag tgggtctgga acagaattta ctctcaccat tagctccctg       60
236     cagccagaag attttgccac ttacttttgc caacagggta atacgcttcc gtggacgttc       120
238 <210> SEQ ID NO: 15
239 <211> LENGTH: 49
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding
244     amino acid 50-65 of the VH region (SEQ ID No. 10). The 3' end of
245     the primer overlaps with the 5'end of the template by 21
246     nucleotides
247 <220> FEATURE:
248 <221> NAME/KEY: primer_bind
249 <222> LOCATION: (1)..(49)
250 <400> SEQUENCE: 15
251     ctacactagt atattacact caggagtccc atcaagggtc agtggcagt           49
253 <210> SEQ ID NO: 16
254 <211> LENGTH: 48
255 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/892,613D

DATE: 10/10/2006  
TIME: 08:43:50

Input Set : N:\Crf4\10022006\I892613C.raw  
Output Set: N:\CRF4\10102006\I892613D.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 15  
Seq#:3; Line(s) 57  
Seq#:4; Line(s) 72  
Seq#:5; Line(s) 87  
Seq#:6; Line(s) 101  
Seq#:7; Line(s) 117  
Seq#:8; Line(s) 132  
Seq#:9; Line(s) 146  
Seq#:11; Line(s) 184  
Seq#:12; Line(s) 199  
Seq#:13; Line(s) 214  
Seq#:14; Line(s) 228  
Seq#:15; Line(s) 243  
Seq#:16; Line(s) 258  
Seq#:17; Line(s) 272  
Seq#:19; Line(s) 314  
Seq#:20; Line(s) 329  
Seq#:21; Line(s) 344  
Seq#:22; Line(s) 358  
Seq#:23; Line(s) 374  
Seq#:24; Line(s) 390  
Seq#:25; Line(s) 404  
Seq#:27; Line(s) 443  
Seq#:28; Line(s) 459  
Seq#:29; Line(s) 474  
Seq#:30; Line(s) 488  
Seq#:31; Line(s) 503  
Seq#:32; Line(s) 518

**VERIFICATION SUMMARY**

DATE: 10/10/2006

PATENT APPLICATION: US/09/892,613D

TIME: 08:43:50

Input Set : N:\Crf4\10022006\I892613C.raw

Output Set: N:\CRF4\10102006\I892613D.raw

L:5 M:270 C: Current Application Number differs, Wrong Format